

Figure 17

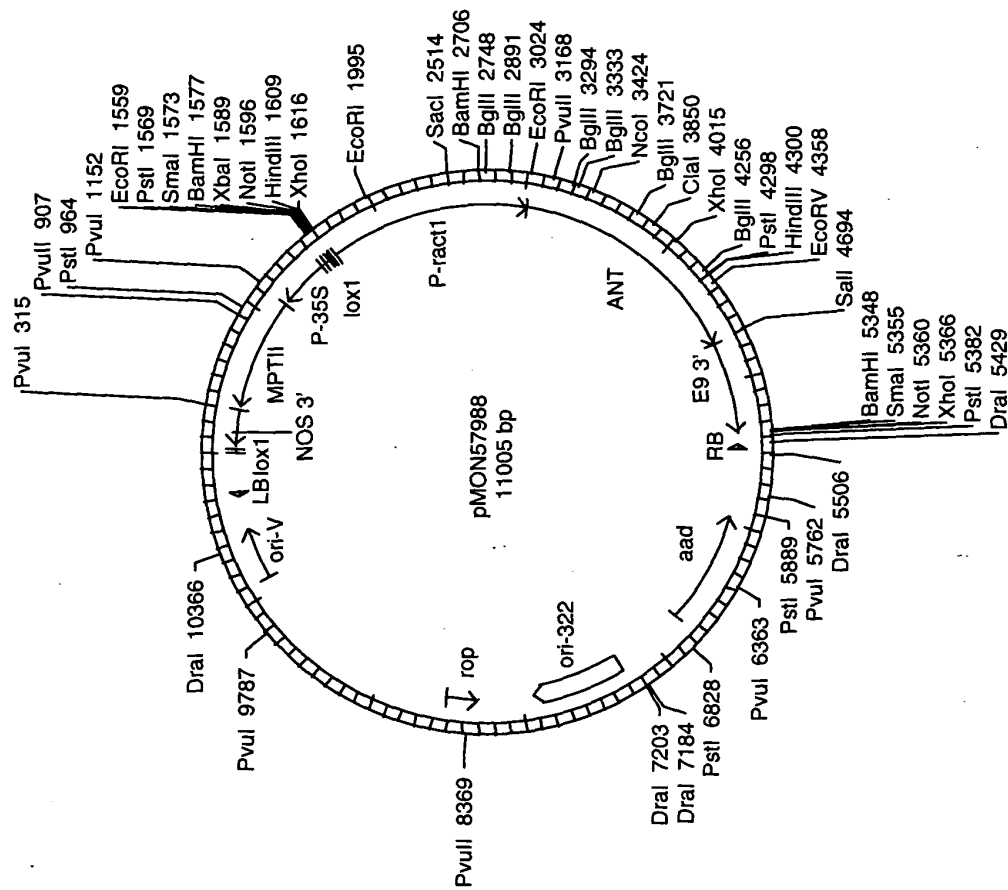


Figure 18

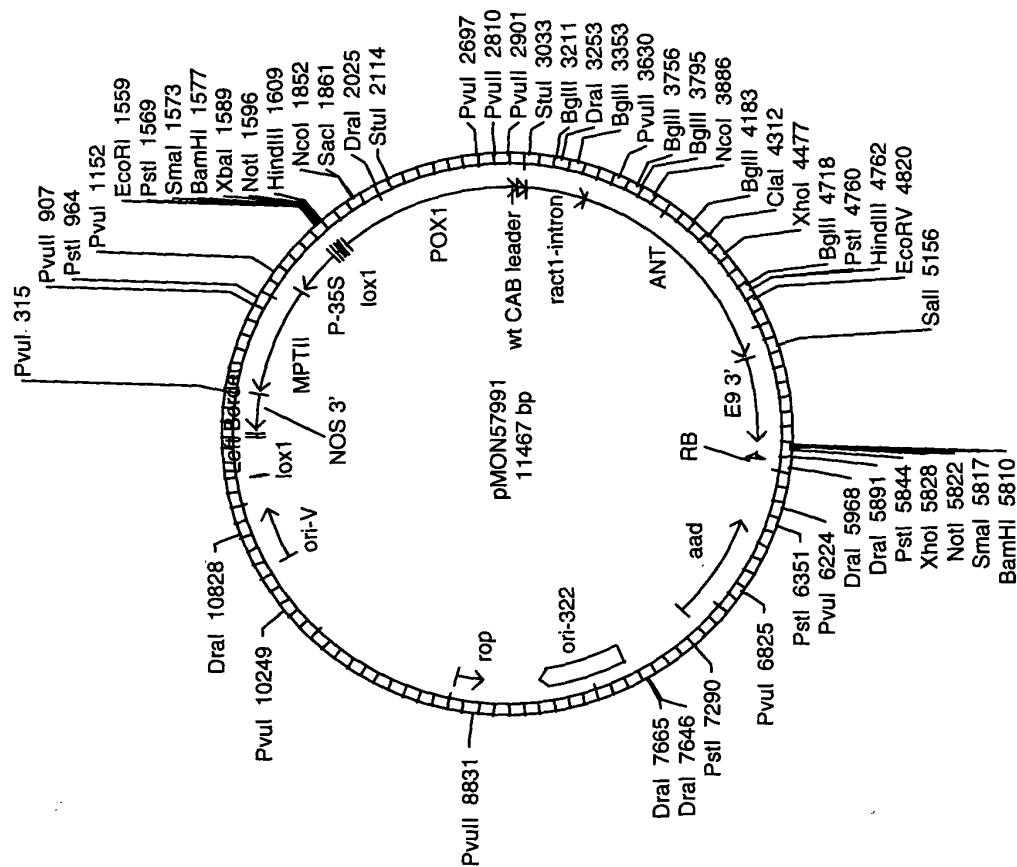
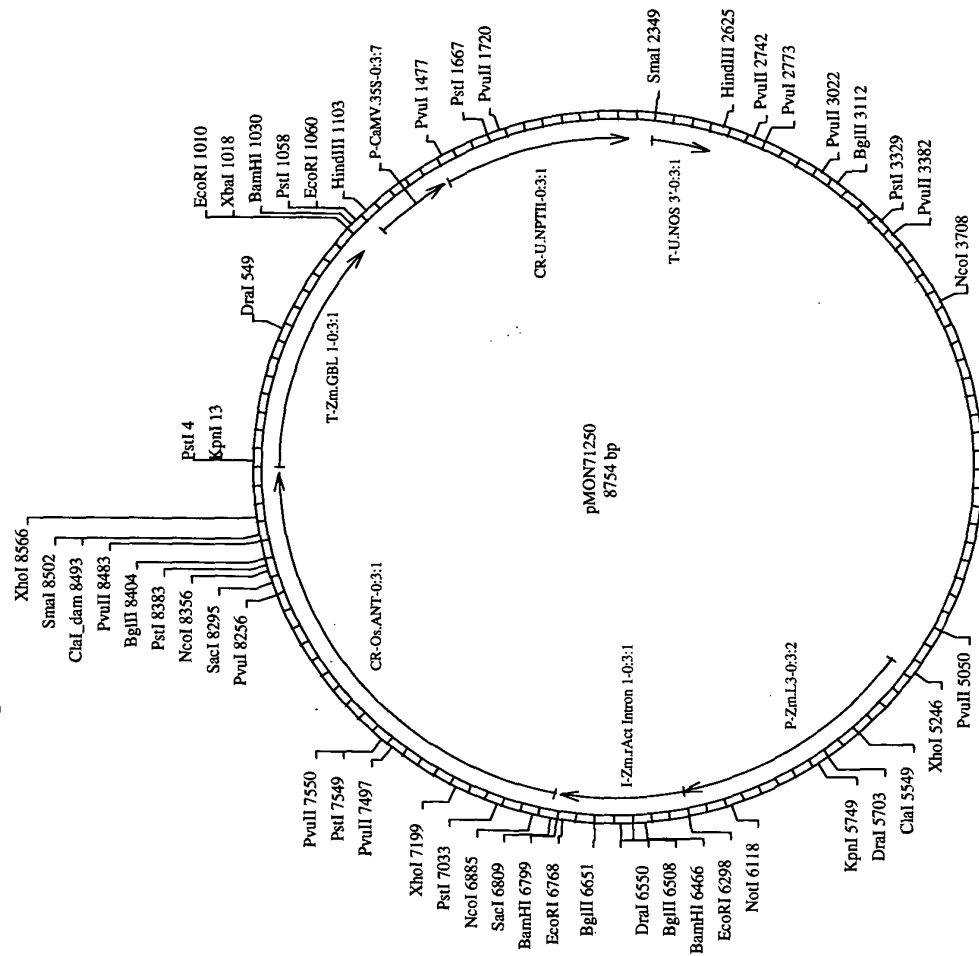


Figure 19



[illegible]

701 T
GmANT1
GmANT2
~
ANT

Figure 2a

g1244708	1	-----MKSFCDNDNNHSTTTLGGFSSNMKKGGRGGRGRIAY-----	40
GmANT1	1	-----MKRINESNTDDNNHLLGGFSSP-HMKKEA-----	31
OsANT2	1	MASGNSSSSSGMAATAGVGGWGGFSP-HMATYCAGGVDDVG-HHHH-----	48
GhANT1	1	-----MSWJGGFSP-HDIODESFEREDHGGF-----	28
GmANT2	1	-----MKSMENDDNADLNQNNWJGGFSPQMHNTGVSSHSPSSAREVWPTSFYHHTAPLSSYGFYY	63
OsANT1	1	-----MASGEGSSWJGGFSPHMPANIEVPSSESPSTAAHH-----HHHPPAA-----	45
g1244708	41	-----SSSTSSAATSSSVPPQLVGGDNTSNFVYCGSNPNG-----IYSHMSV	85
GmANT1	32	-----TSARTVPTTYMSPSL-----SHLSNFVYCYGVGENG-----FHSPLTY	71
OsANT2	49	-----HHVHQHQHGGGLAYN--PAVASSFYGGGHDVAVTSAGGGSYYGGGFSS	99
GhANT1	29	-----	30
GmANT2	64	GLEAENVGLYSALP-----	78
OsANT1	46	-----AAAGAMSSPP-----DSATTCNFLSPPARQVAPSPGYYYGGAYGDDGTSTAGVYY-SHLPM	103
g1244708	86	MPDCSDGSGMBAHNR-----SHSNHQD-----SPKVEFFG-----THN-----	125
GmANT1	72	MPDCSDGSGMBAHNR-----QTQVNVPT-----SPKVEFFG-----TGATMT-----	113
OsANT2	100	MPDCSDGSGMBAHNR-----DDEQGVVWASPKVEFFG-----	137
GhANT1	31	MPDCSDGSGMBAHNR-----SIARDEDURYENGIGSATANEQGPKEFFG-----CCYSNPSQETKAYCGTHEN	98
GmANT2	79	MPDCSDGSGMBAHNR-----DADAMATT-----TPKVEFFG-----GGEAMGTPHHYECSATETMP	133
OsANT1	104	MPDCSDGSGMBAHNR-----	131
g1244708	126	-----NTSHKEAMDLSLSFYN-----TTHPNTTTNFQEFFS-----	159
GmANT1	114	-----HEYGSHERGLSLDSIYMNQNAEQPNRDLLSQPFQQGGMMSVQT	158
OsANT2	138	-----AGPAMALSLSNSAETYYGGHGHQGHQAQDGGAVGGDPHHGG-----	177
GhANT1	99	QNTVPSPTIRINVNAPNYSSSGD-----AEAEENFDPSSF IQTYRYNENPQTLMAGG-----	152
GmANT2	134	LSLDSVFYIQPSRRDPNNQTY-----QNHVQHTSTNQQQQQLQAYYSTLRNHDMLE-----	188
OsANT1	132	-----CGNGSGHDPATYSQGGQEDADASRAYQHHLVP-----	165
g1244708	160	-----FPQTRNHEETRN-YGND-----PSLTHGGSFNVGYGEF-----QQSLSLSMSPGS-----	205
GmANT1	159	HPYYSGLACHLYCAPLEEETTKETHVSDCSSLMPTQTEGLKNWVAPTREFSTHQQVLEQQMNCGMGN	226
OsANT2	178	-----GGFLQCAVIPGAGG-HD-----AALVHDQSSAAVAVAGWAAMHGGGYDIANAARDDV	228
GhANT1	153	-----HSLQCDPNPNHNR-----SG-----VHVVPFESATSVSGFKSWLRATPPGKKASGN-----	201
GmANT2	189	-----CSKQSQTSDNNLHVQNMKG-DDDAVPVPLKSEVRNFQASHAHESKMTVPHVEENAG	245
OsANT1	166	-----YNYPLTEAMLQERAAAP-MEDAMAAA-----KNFLTSTVGACYGNQ-EMPQPLSLSMSP	219
g1244708	206	-QSSCITGSHHQNNQNNHQSNHQIISALVETSGVFETTTAAAKQEDVVVVG	272
GmANT1	227	ERNGVSLGSVECCGLQSLSMSPSSQSSCVTAPS-----GTDSSAVDA	287
OsANT2	229	CAGPIIPTGGHLHPLTSMSSAGSSSCVTVQAARAGEPYMADAYS	294
GhANT1	202	-----ETNNNFDA-SLTMG-----PTSRNGFPATAP-----EVVDN	252
GmANT2	246	ESGSGSMAYEDLSLSMSPS-SGSSSVTSSHRGPAVVDSDVMDT	309
OsANT1	220	GSQSSSCVSAAPQNNQMAVAVAAARAGDGGGSSNDGGEQRVG-----	280

Figure 2b

g1244708	273	DIFGART	QYRG	TRHRWTGRYE	SHJDN	F	KEG	H	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	340	
GmANT1	288	DTEGART	QYRG	TRHRWTGRYE	SHJDN	C	KG	C	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	355	
OsANT2	295	DIFGART	QYRG	TRHRWTGRYE	SHJDN	C	KG	C	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	362	
GmANT1	253	DTEGART	QYRG	TRHRWTGRYE	SHJDN	C	KG	C	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	320	
GmANT2	310	DIFGART	QYRG	TRHRWTGRYE	SHJDN	C	KG	C	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	377	
OsANT1	281	DTEGART	QYRG	TRHRWTGRYE	SHJDN	C	KG	C	RKGRQ	Y	GGYDME	KEAR	YD	LSH	KYM	348	
g1244708	341	G	THNFSAN	Y	K	E	M	M	Y	R	E	Y	H	L	R	R	555
GmANT1	356	G	THNFSAN	Y	V	E	M	M	Y	R	E	Y	H	L	R	R	555
OsANT2	363	G	THNFSAN	Y	E	E	M	M	Y	R	E	Y	H	L	R	R	555
ZmANT1	1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	37
GmANT1	321	G	THNFSAN	Y	K	E	M	M	Y	R	E	Y	H	L	R	R	555
GmANT2	378	G	THNFSAN	Y	N	E	M	M	Y	R	E	Y	H	L	R	R	555
OsANT1	349	G	THNFSAN	Y	D	E	M	M	Y	R	E	Y	H	L	R	R	555
g1244708	409	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	462
GmANT1	424	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	477
OsANT2	431	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	498
ZmANT1	38	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	91
GmANT1	389	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	442
GmANT2	446	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	499
OsANT1	417	KDLYLGTFG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	470
g1244708	463	RR	---	---	---	---	---	---	---	---	---	---	---	---	---	---	475
GmANT1	478	RR	RRKKNDPRNK	IDY	NSVAT	V	NNEET	VQ	QAG	NNNN	ENDSE	V	ML	FN	HP	S	545
OsANT2	499	RR	KGKVG	---	---	---	---	---	---	---	---	---	---	---	---	---	553
ZmANT1	92	QVRR	---	---	---	---	---	---	---	---	---	---	---	---	---	---	141
GmANT1	443	KASP	---	---	---	---	---	---	---	---	---	---	---	---	---	---	495
GmANT2	500	RRNRET	NETQ	ICD	GNHNKPS	Y	EDT	Q	EAL	IM	HQ	KSC	ES	EN	QW	Y	567
OsANT1	471	A	RVKKAIEA	PD	HP	IGR	ELG	TE	AS	AT	Y	---	---	---	---	---	529
g1244708	476	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	499
GmANT1	546	IMNC	GN	Y	NS	A	F	S	M	A	D	L	I	G	D	S	611
OsANT2	554	GGH	QH	D	L	P	S	D	A	F	S	M	A	D	I	G	608
ZmANT1	142	QQRQD	---	---	---	---	---										

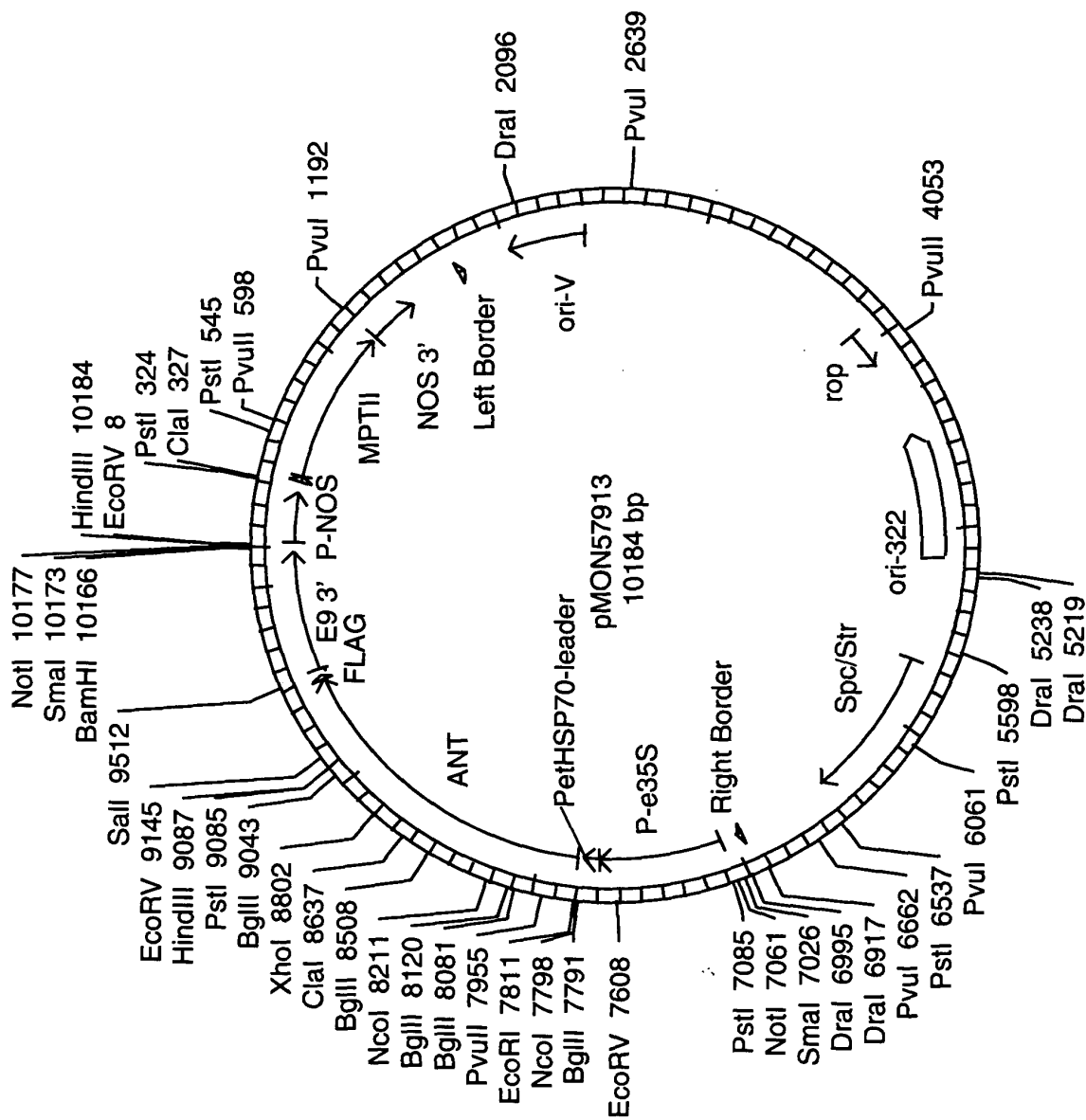


Figure 4

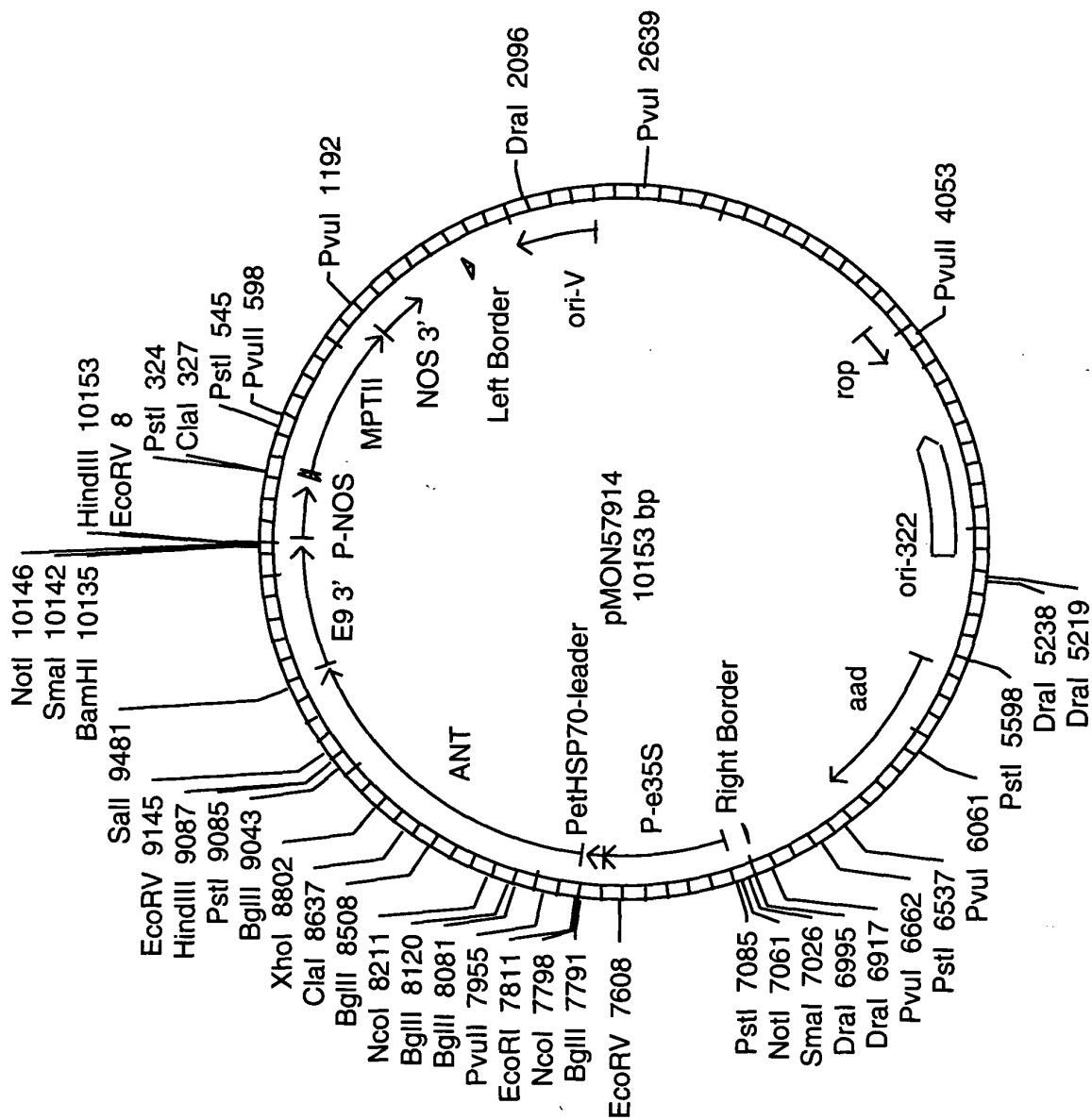
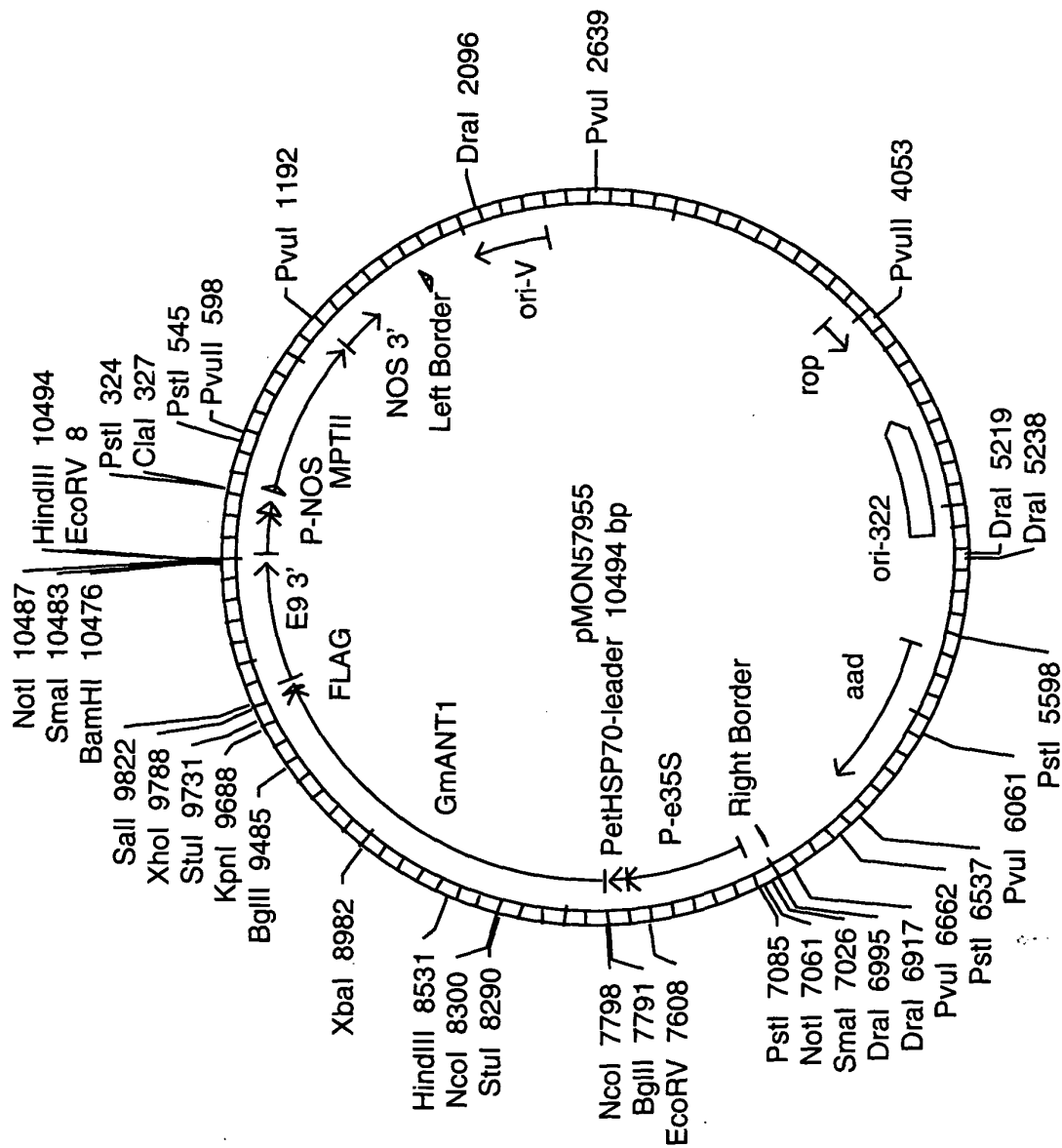


Figure 5

Figure 6



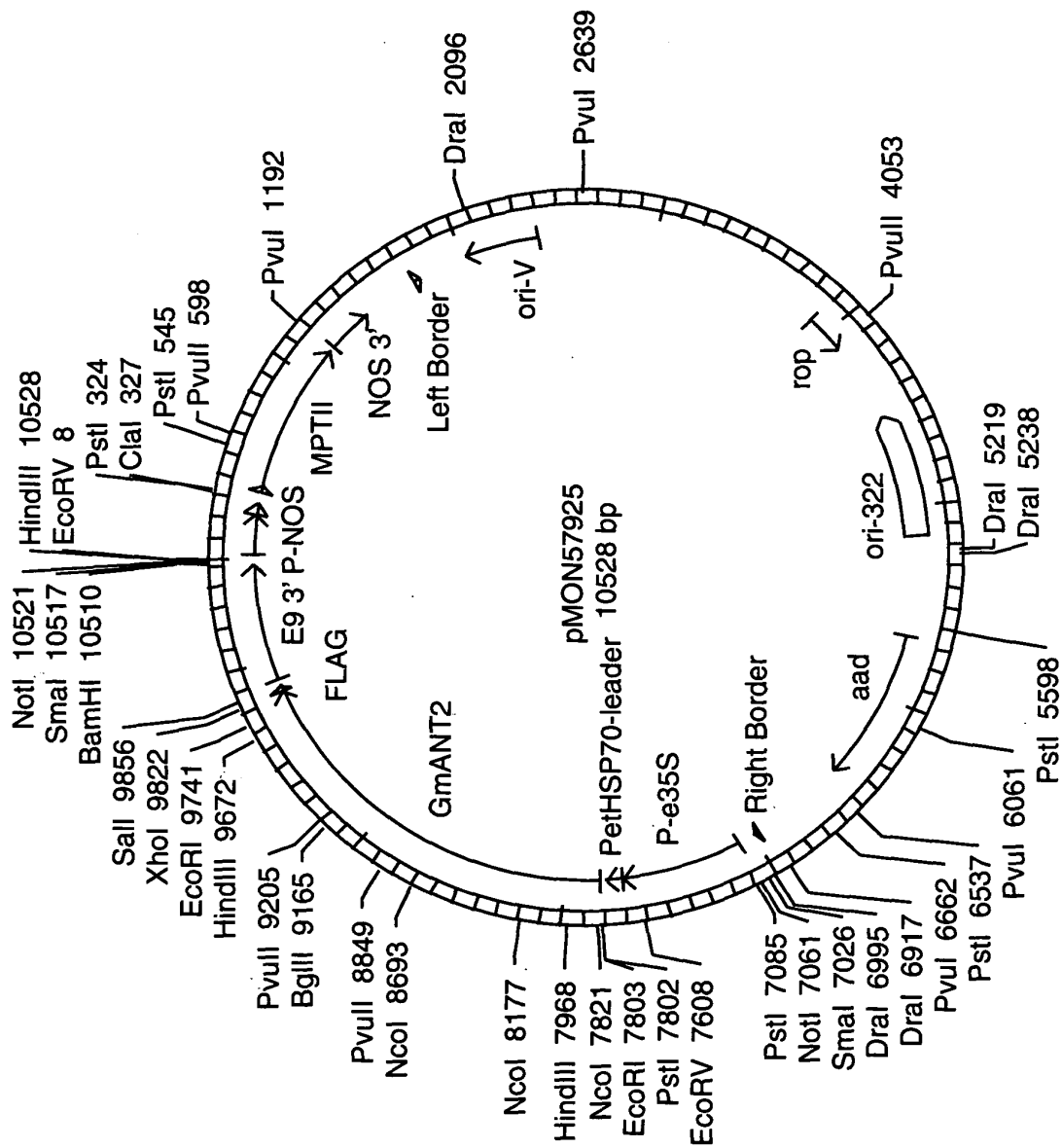


Figure 7

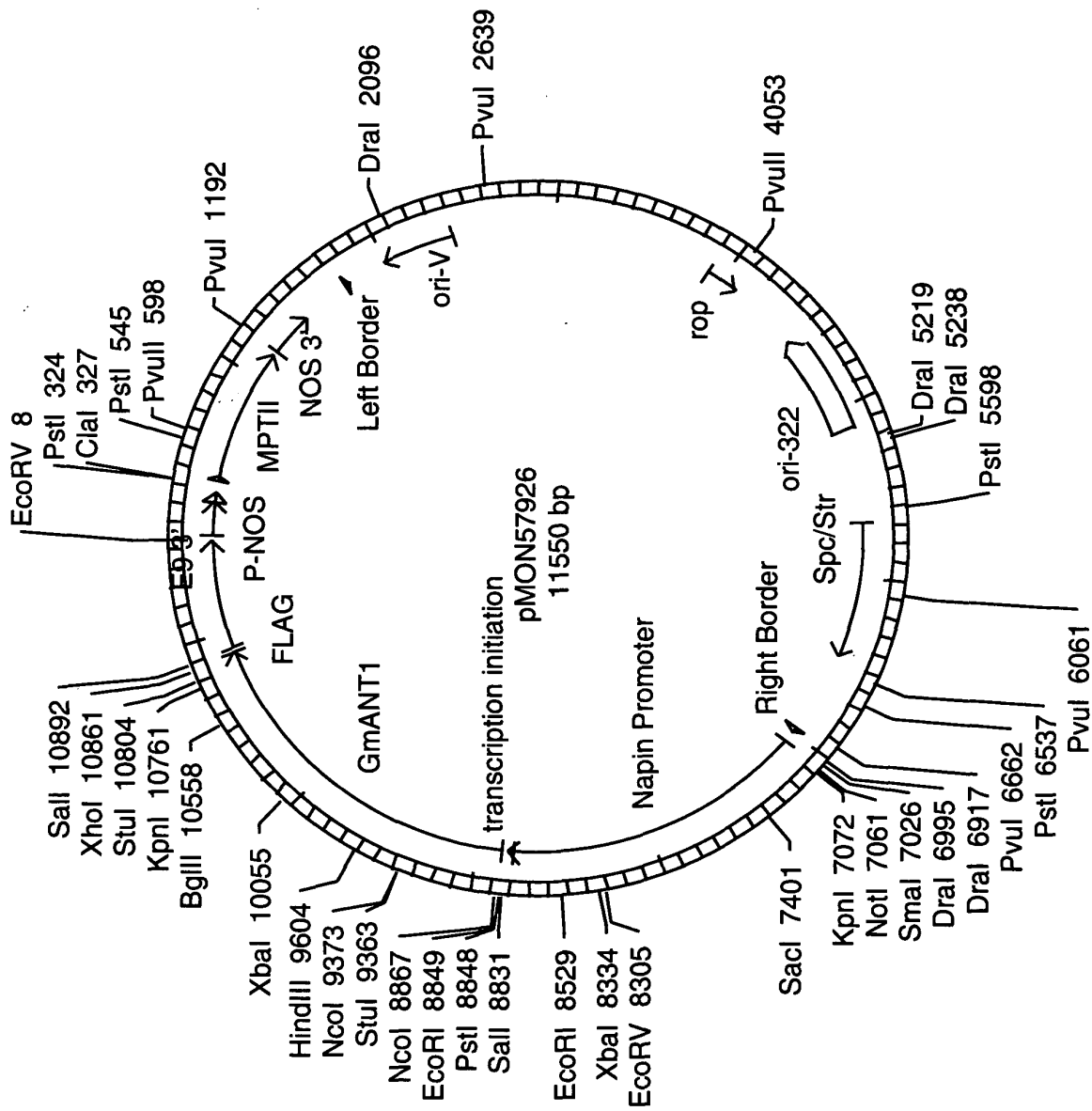


Figure 8

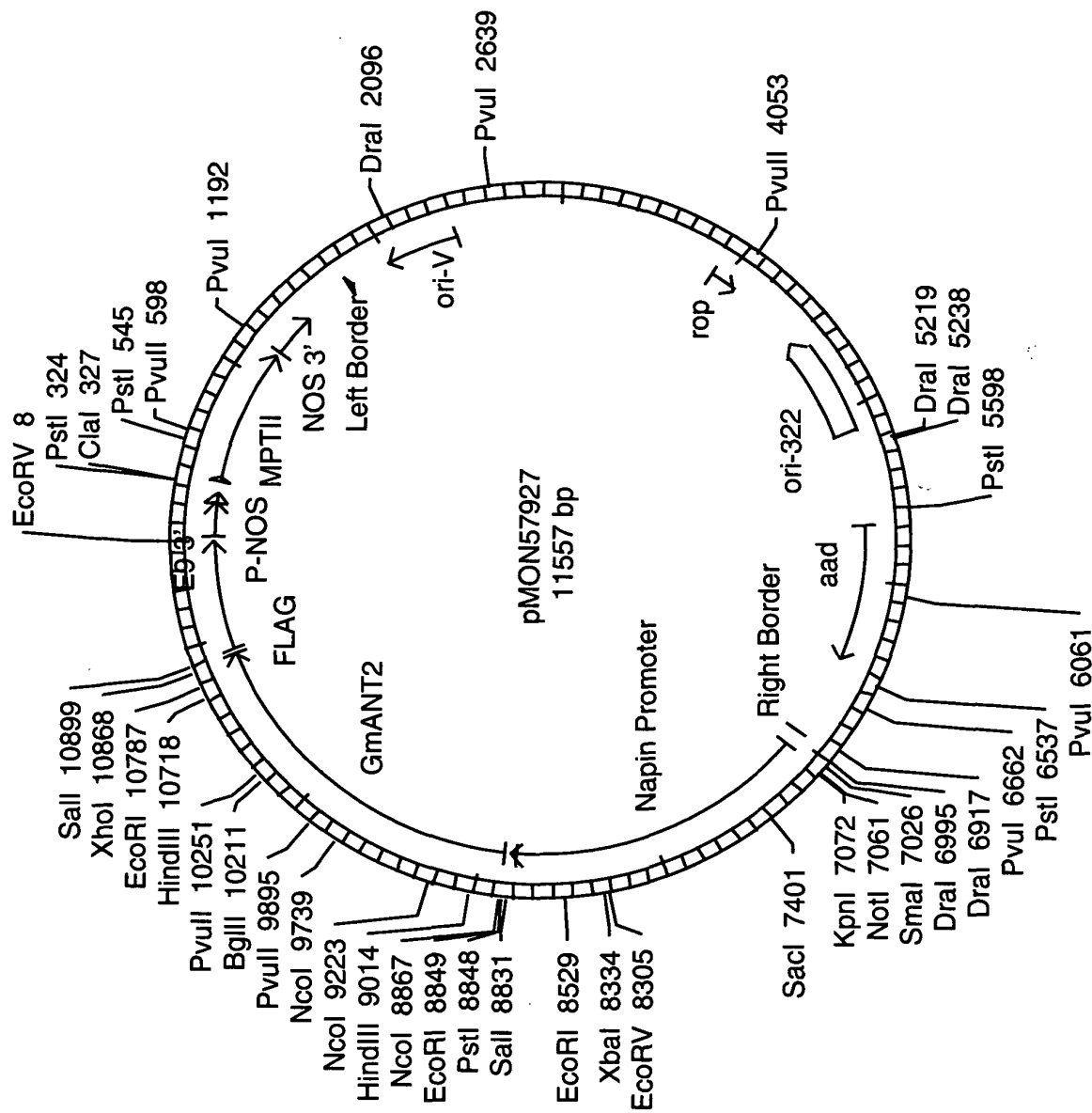
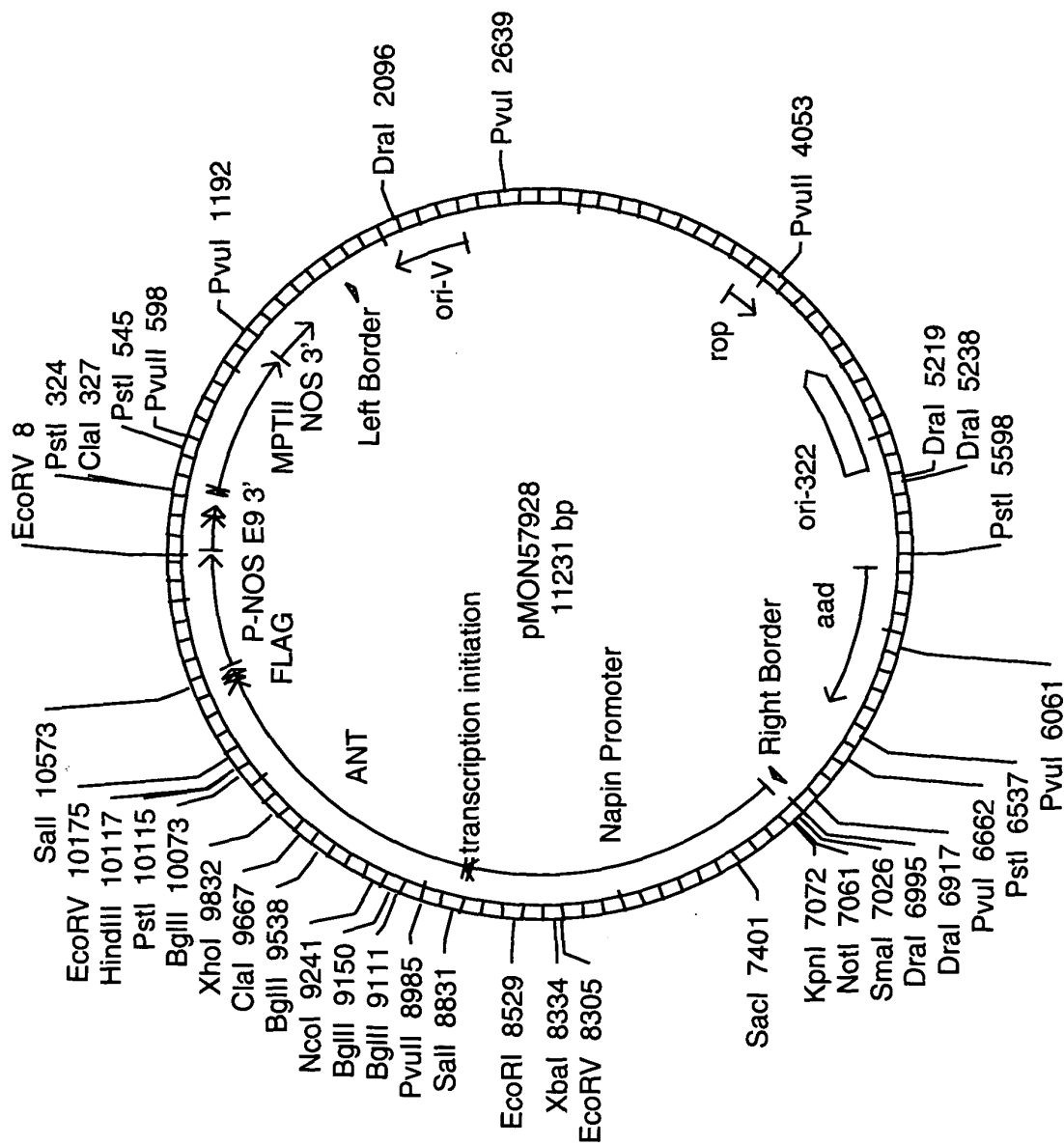


Figure 9

Figure 10



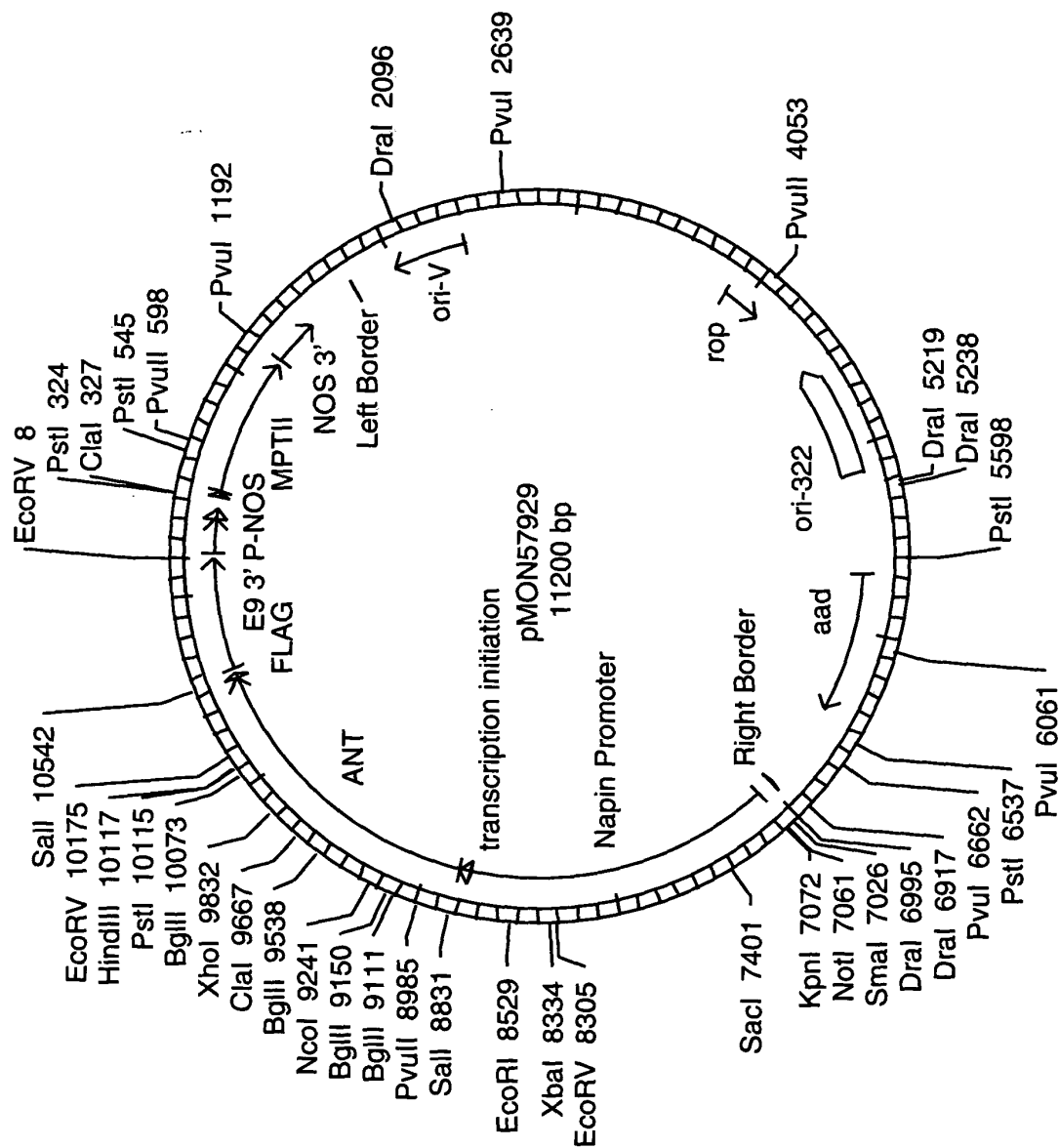


Figure 11

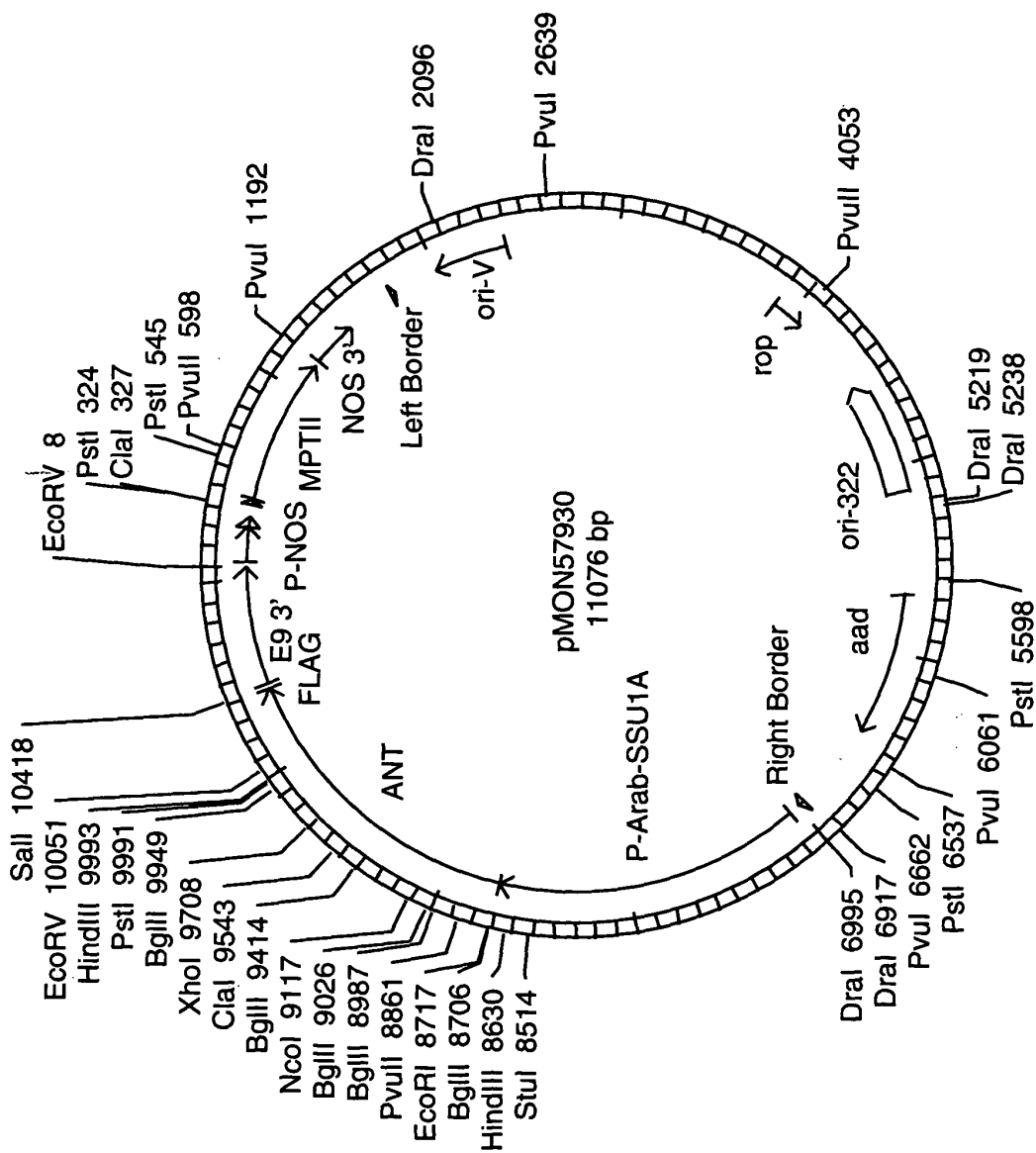


Figure 12

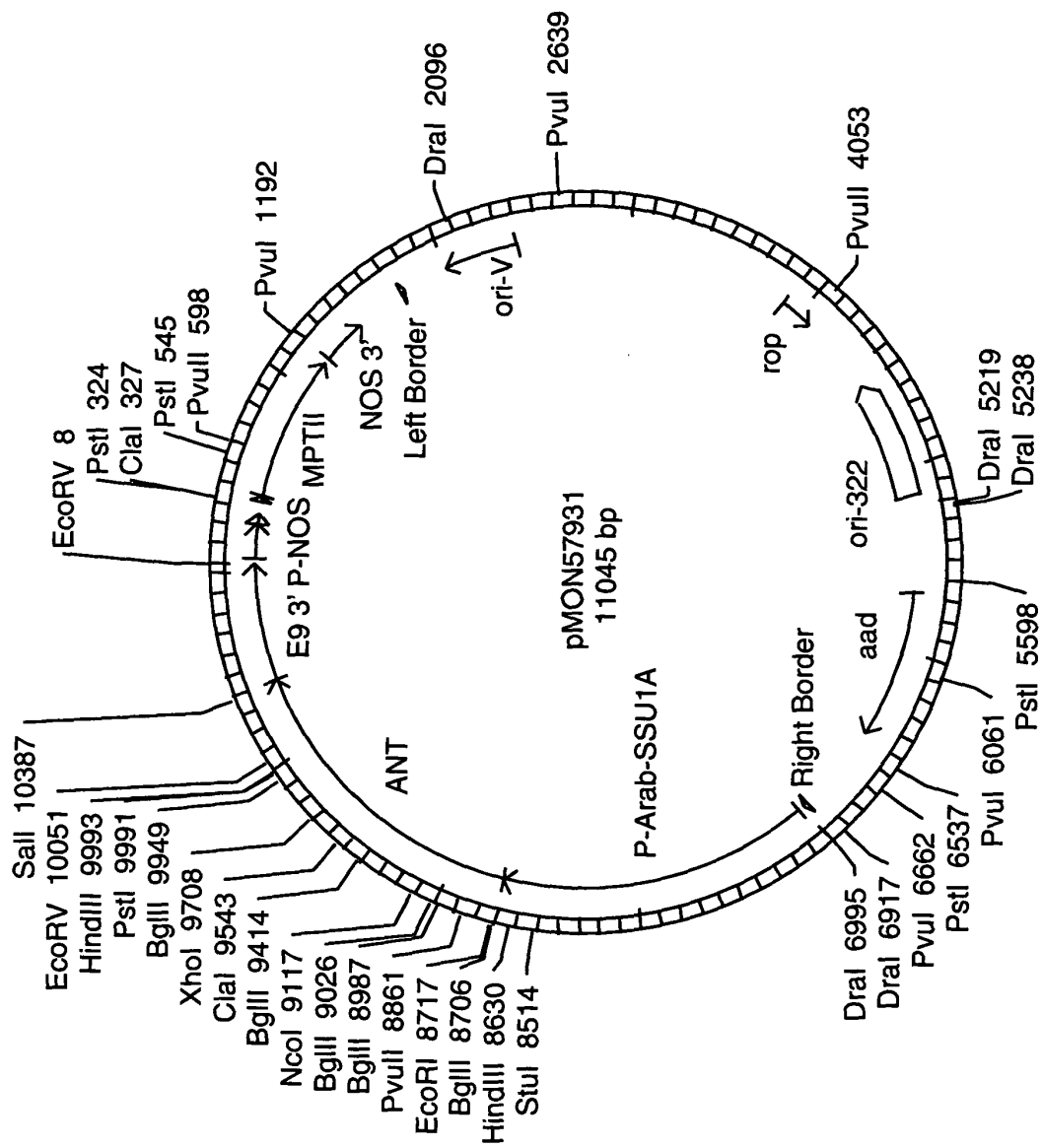


Figure 14

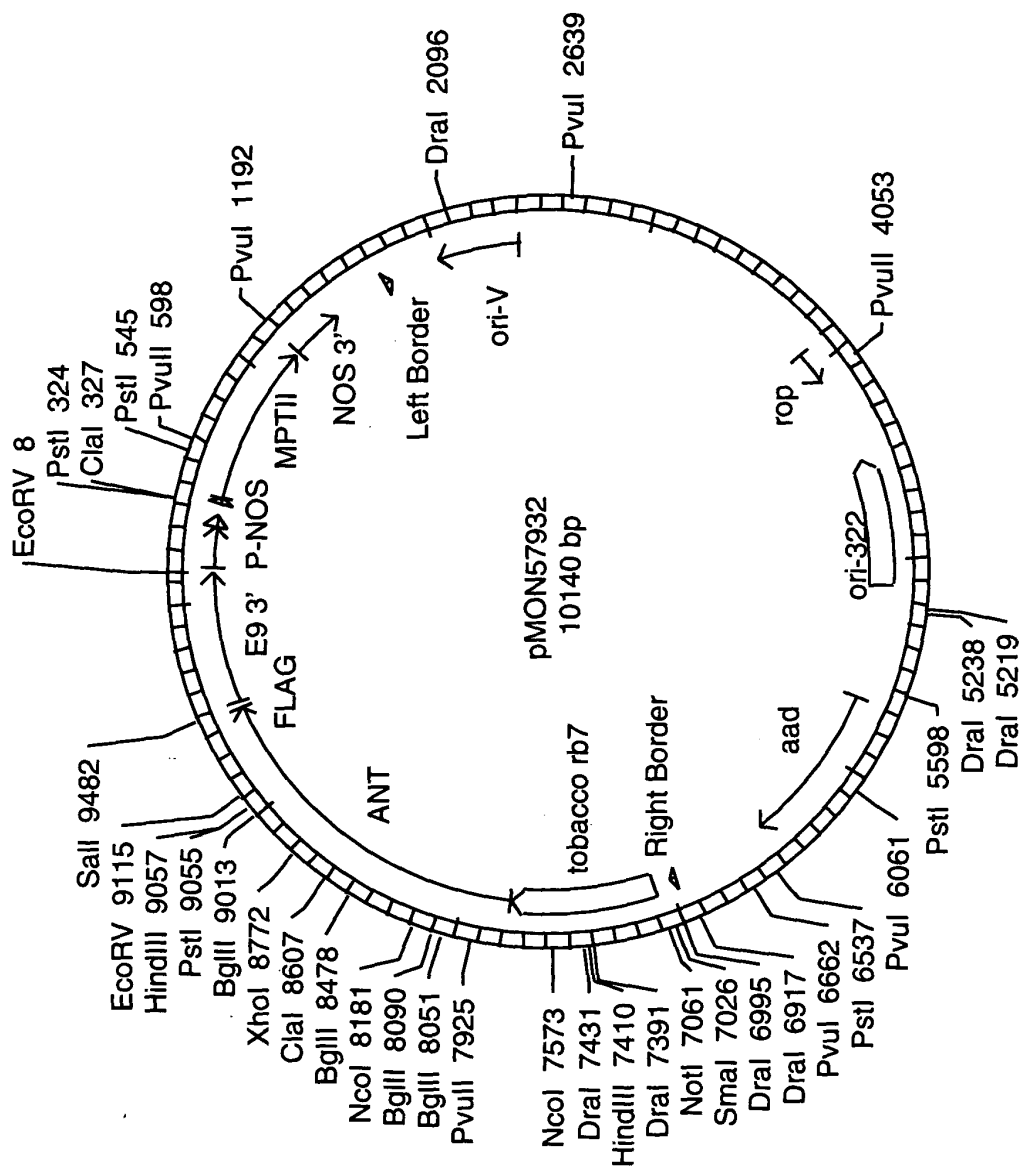


Figure 15

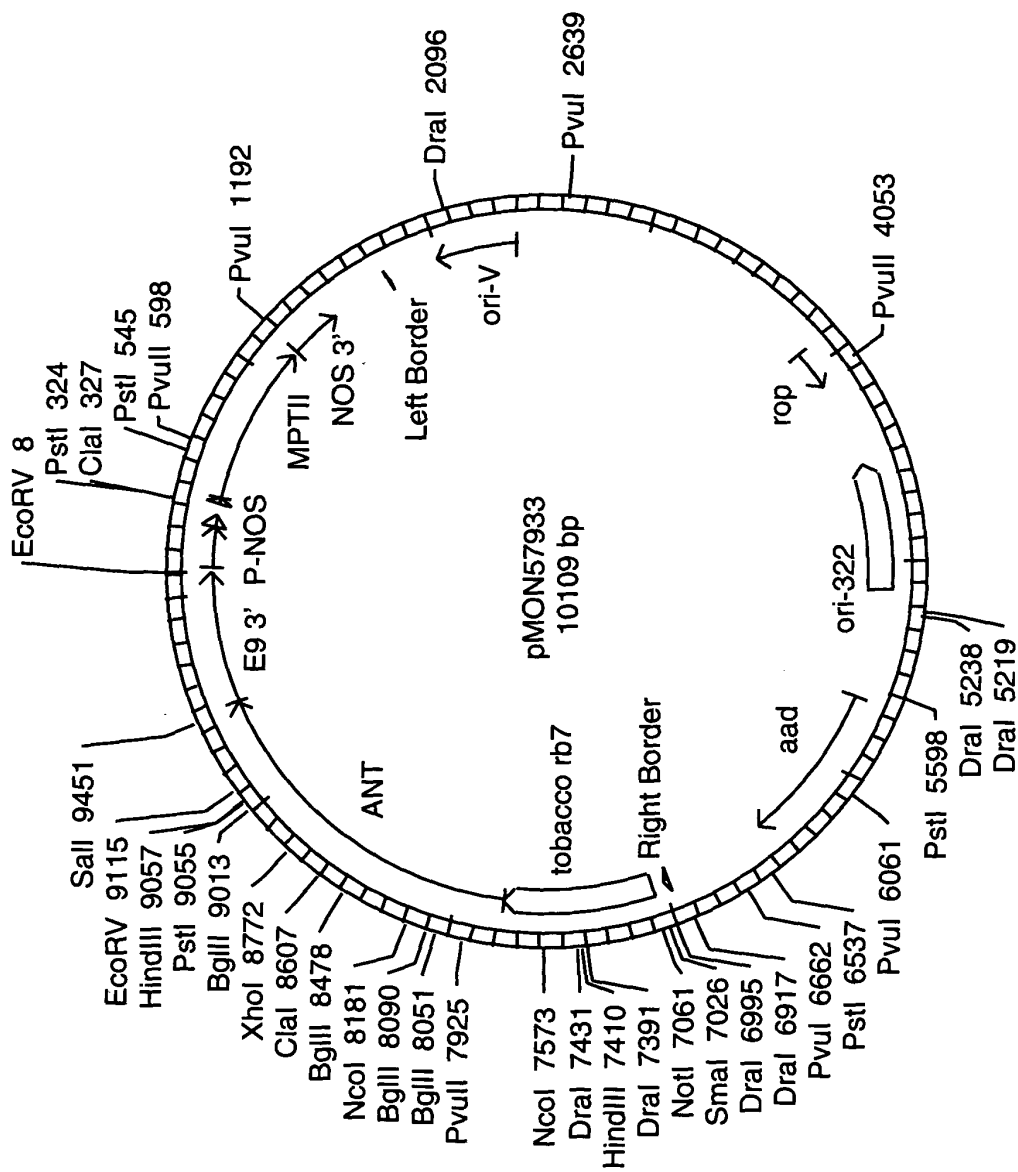


Figure 16

